

STIC-Biotech/ChemLib

178579

From: Sullivan, Daniel  
Sent: Friday, February 03, 2006 2:42 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search request 09846456

Please search for the following in the issued patent and commercial databases:

An oligo search of SEQ ID-NO: 1, 2, 3 and 5

Thank you.

**Daniel M. Sullivan**

Examiner AU 1636  
Remsen Bldg.  
Room 2A74

Tel: (571) 272-0779

Mailbox: 2C70

RECEIVED  
FEB - 3 2006  
STIC

Oligo search was not done, per our  
phone conversation. To do the regular  
plus oligo searches would add up  
to about 28 hrs, and our limit w/o  
special permission is 20 hours.

If these results are not adequate, we can  
figure out how to proceed. Let me know  
if you require further work.  
Mary Jane Rahl  
Ext. 22526

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model  
Run on: February 8, 2006, 23:04:12 : Search time 546.227 Seconds  
(without alignments)  
16546.426 Million cell updates/sec

Title: US-09-846-456A-5  
Perfect score: 159  
Sequence: 1 ttaatgaccacccagggcg.....ctttcagaagagacaaaca 159

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

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- 1: gb\_ba.\*
- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_sts.\*
- 11: gb\_sv.\*
- 12: gb\_un.\*
- 13: gb\_vi.\*
- 14: gb\_hcg.\*
- 15: gb\_pi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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5	155.8	98.0	10442	6	CS108251	Sequence
6	155.8	98.0	10442	6	AR607250	Sequence
7	155.8	98.0	10442	6	AR628825	Sequence
8	155.8	98.0	10442	6	AX060713	Sequence
9	155.8	98.0	10442	6	AX060892	Sequence
10	155.8	98.0	10442	8	AF285167	Sequence
11	155.8	98.0	10474	6	AR607255	Sequence
12	155.8	98.0	10474	6	AR607256	Sequence
13	155.8	98.0	10474	6	AR628830	Sequence
14	155.8	98.0	10474	6	AR628831	Sequence
15	155.8	98.0	10474	6	AX060719	Sequence
16	155.8	98.0	10474	6	AX060721	Sequence
17	155.8	98.0	10474	6	AX060898	Sequence
18	155.8	98.0	10474	6	AX060900	Sequence

19	155.8	98.0	149034	8	AF275948	Homo sapi
20	153.2	96.4	183999	6	AX092589	Sequence
21	143.4	90.2	697	8	AF258627	Homo sapi
22	142.2	89.4	200	8	AF258624	Homo sapi
23	142.2	89.4	446	6	AX127764	Sequence
24	142.2	89.4	446	6	AX139751	Sequence
25	142.2	89.4	447	6	BD117945	EST and e
26	142.2	89.4	447	6	AR422392	Sequence
27	142.2	89.4	447	6	AX983086	Sequence
28	142.2	89.4	480	8	HSA252277	Homo sapi
29	142.2	89.4	1062	6	AR583753	Sequence
30	142.2	89.4	1062	6	AX616417	Sequence
31	142.2	89.4	7260	6	AX253452	Sequence
32	142.2	89.4	9741	6	AX127830	Sequence
33	142.2	89.4	9741	6	AX139817	Sequence
34	142.2	89.4	9741	6	AX351038	Sequence
35	142.2	89.4	9854	6	AX127831	Sequence
36	142.2	89.4	9854	6	AX139818	Sequence
37	142.2	89.4	10412	6	CQ785966	Sequence
38	142.2	89.4	10412	6	CQ981355	Sequence
39	142.2	89.4	10412	6	CS031387	Sequence
40	142.2	89.4	10412	6	CS036636	Sequence
41	142.2	89.4	10412	6	CS040339	Sequence
42	142.2	89.4	10412	6	CS045588	Sequence
43	142.2	89.4	10545	6	AR393492	Sequence
C 44	142.2	89.4	129608	8	AL353685	Human DNA
C 45	142.2	89.4	175064	14	AC012230	Homo sapi

## ALIGNMENTS

RESULT 1  
AX351033  
LOCUS AX351033 159 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 5 from Patent WO0183746.  
ACCESSION AX351033  
VERSION AX351033.1 GI:18616389  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Rosier-Montus, M.F., Prades, C., Lemoine C., Naudin, L., Deneffe, P.,  
Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.  
TITLE Regulatory nucleic acid sequences of the abci gene  
JOURNAL Patent: WO 0183746-A 5 08-NOV-2001;  
Aventis Pharma S.A. (FR)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN	Query Match	Best Local Similarity	Score	DB	Length
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Qy 61	GAGCCACACGCTGGGCGTGTGGCTGAGGGAACATGGCATGTGGCCCTCAGTGAAGTTG	120			
Db 61	GAGCCACACGCTGGGCGTGTGGCTGAGGGAACATGGCATGTGGCCCTCAGTGAAGTTG	120			
Qy 121	CTGCTGTGGAAGAACCTCCTTCAGTTCAGAGAGACAAACA	159			
Db 121	CTGCTGTGGAAGAACCTCCTTCAGTTCAGAGAGACAAACA	159			

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Run on: February 8, 2006, 17:12:15 ; Search time 65.9706 Seconds  
(without alignments)  
16062.998 Million cell updates/sec

Title: US-09-846-456A-5

Perfect score: 159

Sequence: 1 ttaatgaccagccacggcg.....ctttcagaagaacaaca 159

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001as.\*  
5: Geneseq2001bs.\*  
6: Geneseq2002as.\*  
7: Geneseq2002bs.\*  
8: Geneseq2003as.\*  
9: Geneseq2003bs.\*  
10: Geneseq2003cs.\*  
11: Geneseq2003ds.\*  
12: Geneseq2004as.\*  
13: Geneseq2004bs.\*  
14: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	100.0	159	6	AAD37269 Human ABC
2	159	100.0	357	6	AAD37266 Human ABC
3	159	100.0	357	6	ABL58148 Human ABC
4	157.4	99.0	159	6	ABN99235 Polymorph
5	155.8	98.0	10365	10	ADD94068 Human ATP
6	155.8	98.0	10381	10	ADD94069 Human ATP
7	155.8	98.0	10423	10	ADD94070 Human ATP
8	155.8	98.0	10442	4	Aaf24680 Nucleotid
9	155.8	98.0	10442	4	Aaf24702 Nucleotid
10	155.8	98.0	10442	13	ADP23549 PRO polyp
11	155.8	98.0	10442	14	ADY15089 DNA encod
12	155.8	98.0	10442	14	AEA23717 Human PRO
13	155.8	98.0	10474	4	AAF24685 Nucleotid
14	155.8	98.0	10474	4	AAF24686 Nucleotid
15	155.8	98.0	10474	4	AAF24708 Nucleotid
16	155.8	98.0	10474	4	AAF24707 Nucleotid
17	155.8	98.0	149034	11	ADP65433 Human ABC
18	153.2	96.4	183999	4	AAF92831 Human ABC
19	153.2	96.4	183999	13	ADU76470 Human ABC

20	147	92.5	158	6	ABN99234	Abn99234 Polymorph
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22	143.4	90.2	201	13	ADQ44225	Adq44225 Myocardia
23	143.4	90.2	201	13	ADQ44200	Adq44200 Myocardia
24	143.4	90.2	1402	13	ADQ38534	Adq38534 Human SNP
25	143.4	90.2	1859	13	ADQ38532	Adq38532 Human SNP
26	143.4	90.2	10405	13	ADQ38535	Adq38535 Human SNP
27	142.2	89.4	446	4	AAS04035	Aas04035 Partial h
28	142.2	89.4	1062	8	ACC51110	Acc51110 Human HAB
29	142.2	89.4	7086	4	ABA09200	Aba09200 Human ABC
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31	142.2	89.4	7260	4	AAI70315	Aai70315 Human ATP
32	142.2	89.4	7260	4	AAD21326	Aad21326 Human ATP
33	142.2	89.4	7281	4	AAS1683	Aas1683 Human pol
34	142.2	89.4	9741	4	AAS06120	Aas06120 Human ABC
35	142.2	89.4	9741	6	ABD37273	Abd37273 Human ABC
36	142.2	89.4	9741	6	ABL58146	AbL58146 Human ABC
37	142.2	89.4	9854	4	AAS06121	Aas06121 Human ABC
38	142.2	89.4	9870	6	ABN99307	Abn99307 Polymorph
39	142.2	89.4	9870	6	ABN99302	Abn99302 Polymorph
40	142.2	89.4	9870	6	ABN99305	Abn99305 Polymorph
41	142.2	89.4	9870	6	ABN99317	Abn99317 Polymorph
42	142.2	89.4	9870	6	ABN99321	Abn99321 Polymorph
43	142.2	89.4	9870	6	ABN99323	Abn99323 Polymorph
44	142.2	89.4	9870	6	ABN99309	Abn99309 Polymorph
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## ALIGNMENTS

### RESULT 1

AAD37269

ID AAD37269 standard; DNA; 159 BP.

XX

AC AAD37269;

XX 21-AUG-2002 (first entry)

XX Human ABC1 gene exon 1B DNA.

XX Human; ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis;

KW cholesterol metabolism; hypercholesterolaemia; antisense therapy;  
exon 1B; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 94..159

FT /\*tag= a

FT /product= "Protein encoded by human ABC1 gene exon 1B"

FT /note= "CDS does not include stop codon"

FT /partial

XX WO200183746-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-EP005488.

XX 02-MAY-2000; 2000US-0201280P.

XX (AVET ) AVENTIS PHARMA SA.

XX Rosier-Montus M, Prades C, Lemoine C, Naudin L, Deneffe P;

XX Brewer B, Duverger N, Remaley A, Santamarina-Fejo S;

XX WPI; 2002-154404/20.

XX P-PSDB; AAE22999.

XX Isolated nucleic acid useful for modifying the ATP-binding cassette 1

XX (ABC1) and screening for candidate modulatory compounds or substances.

XX

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OM nucleic - nucleic search, using sw model  
Run on: February 9, 2006, 15:01:42 ; Search time 444.338 Seconds  
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16742.090 Million cell updates/sec

Title: US-09-846-456A-5  
Perfect score: 159  
Sequence: 1 ttaataaccagccacggcg.....ctttcagaagaacaaaca 159

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: gb\_est3.\*  
4: gb\_est4.\*  
5: gb\_est5.\*  
6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_gss1.\*  
10: gb\_gss2.\*  
11: gb\_gss3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155.8	98.0	547	1 AL698654	AL698654 DKFP686N12109
2	155.8	98.0	583	3 BP280727	BP280727 BP280727
3	155.8	98.0	595	3 BP280045	BP280045 BP280045
4	142.2	89.4	583	3 BP200657	BP200657 BP200657
5	142.2	89.4	583	3 BP287529	BP287529 BP287529
6	142.2	89.4	663	5 BX955241	BX955241 DKFP781F
7	140.6	88.4	736	1 AU135588	AU135588 AU135588
8	105.4	66.3	648	9 B2865821	B2865821 CH240 259
9	72.8	45.8	619	2 B657864	B657864 B657864
10	72.8	45.8	4783	4 AK051920	AK051920 Mus muscu
11	70.8	44.5	292	8 Z44377	Z44377 HSC12B081 n
12	70.8	44.5	535	2 BG384217	BG384217 303216 MA
13	54	34.0	490	8 DN853427	DN853427 4149571 B
14	44.8	28.2	668	8 CX260141	CX260141 1313535 N
15	44.8	28.2	742	5 BX911478	BX911478 BX911478
16	44	27.7	862	7 CO927141	CO927141 AGENCOURT
17	43.4	27.3	641	3 BJ901916	BJ901916 BJ901916
18	42.6	26.8	1284	4 CNS0EXH	CR645863 Tetraodon
19	40	25.2	340	5 BY175500	BY175500 BY175500
20	39.8	25.0	696	7 CO358299	CO358299 DR ATE OR
21	38.4	24.2	605	1 AJ732100	AJ732100 AJ732100
22	38.4	24.2	687	1 AJ732095	AJ732095 AJ732095

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	24	36.6	23.0	640	5	BW197209	BW197209 BW197209
	25	36.4	22.9	250	5	BY197692	BY197692 BY197692
	26	36	22.6	520	1	AV955395	AV955395 AV955395
C	27	36	22.6	533	1	AV845237	AV845237 AV845237
	28	36	22.6	587	5	BW325075	BW325075 BW325075
	29	36	22.6	623	5	BW343397	BW343397 BW343397
	30	36	22.6	651	5	BW035269	BW035269 BW035269
	31	36	22.6	685	5	BW251404	BW251404 BW251404
	32	35.6	22.4	514	9	BH087817	BH087817 RBCI-24-3
	33	35.4	22.3	482	9	AQ848626	AQ848626 LMAJFV1_1
C	34	35	22.0	571	1	AV862022	AV862022 AV862022
C	35	35	22.0	579	6	CA243705	CA243705 SCQGLA07
C	36	35	22.0	963	5	BQ944075	BQ944075 AGENCOURT
	37	34.8	21.9	301	1	AW751638	AW751638 RCS-CT007
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	40	34.8	21.9	358	5	BY177088	BY177088 BY177088
	41	34.8	21.9	358	5	BY210952	BY210952 BY210952
	42	34.8	21.9	365	2	BB843149	BB843149 BB843149
	43	34.8	21.9	367	5	BY213387	BY213387 BY213387
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	45	34.8	21.9	516	2	BF484412	BF484412 WHE2323_B

ALIGNMENTS

RESULT 1  
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LOCUS DKFP686N12109\_r1 686 (synonym: hicc3) Homo sapiens CDNA clone  
DEFINITION DKFP686N12109 5', mRNA sequence.  
ACCESSION AL698654  
VERSION AL698654.1 GI:19619194  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 547)  
AUTHORS Dueterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
TITLE EST (Dueterhoeft, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS  
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Olagen (Hilden/Germany) within the CDNA sequencing consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFP686N12109) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.  
Location/Qualifiers  
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/lab\_host="DH10B"  
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Query Match 98.0%; Score 155.8; DB 1; Length 547;  
Best Local Similarity 98.7%; Pred. No. 3.1e-33;

Result No.	Query			DB	ID.	Description
	Score	Match	Length			
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2	159	100.0	357	3	US-09-846-456-2	Sequence 2, Appli
3	159	100.0	357	3	US-09-984-827-4	Sequence 4, Appli
4	157.4	99.0	159	3	US-09-984-827-26	Sequence 26, Appli
5	155.8	98.0	10365	5	US-10-098-939-1	Sequence 1, Appli
6	155.8	98.0	10381	5	US-10-098-939-2	Sequence 2, Appli
7	155.8	98.0	10423	5	US-10-098-939-3	Sequence 3, Appli
8	155.8	98.0	10442	8	US-10-920-989-1	Sequence 1, Appli
9	155.8	98.0	10442	9	US-10-972-836-1	Sequence 1, Appli
10	155.8	98.0	10474	8	US-10-920-989-7	Sequence 7, Appli
11	155.8	98.0	10474	8	US-10-920-989-9	Sequence 9, Appli
12	155.8	98.0	10474	9	US-10-972-836-7	Sequence 7, Appli
13	155.8	98.0	10474	9	US-10-972-836-9	Sequence 9, Appli
14	155.8	98.0	149033	8	US-10-287-436A-956	Sequence 956, App
15	153.2	96.4	183999	7	US-10-745-377-1	Sequence 1, Appli
16	153.2	96.4	183999	8	US-10-872-113-1	Sequence 1, Appli
17	147	92.5	158	3	US-09-984-827-25	Sequence 25, Appli
18	143.4	90.2	201	8	US-10-719-993-1710	Sequence 1710, Ap
19	143.4	90.2	201	8	US-10-719-993-1768	Sequence 1768, Ap
20	143.4	90.2	201	8	US-10-719-993-1793	Sequence 1793, Ap
21	143.4	90.2	201	8	US-10-719-993-10219	Sequence 10219, A
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23	143.4	90.2	201	8	US-10-741-600-5863	Sequence 5863, Ap

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 22:47:42 ; Search time 42.2643 Seconds  
(without alignments)  
3382.690 Million cell updates/sec

Title: US-09-846-456A-5  
Perfect score: 159  
Sequence: 1 ttaatgaccacccggcg.....ctttcagaagaagacaaaca 159

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:

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- 2: /cgn2\_6/ptodata/1/pubpna/US06 NEW PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US07 NEW PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/ECT NEW PUB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US09 NEW PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10 NEW PUB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10 NEW PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US60 NEW PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	143.4	90.2	201	7	US-10-995-561-3388
2	143.4	90.2	201	7	US-10-995-561-3388
3	143.4	90.2	201	7	US-10-995-561-3411
4	143.4	90.2	201	7	US-10-995-561-3429
5	143.4	90.2	201	7	US-10-995-561-23954
6	143.4	90.2	1402	7	US-10-995-561-85
7	143.4	90.2	1859	7	US-10-995-561-84
8	143.4	90.2	10405	7	US-10-995-561-83
9	142.2	89.4	159138	7	US-10-995-561-13230
10	64.4	40.5	6786	11	US-11-055-309A-7
11	57	35.8	201	7	US-10-995-561-24507
12	34.6	21.8	6768	11	US-11-043-889-1
13	34.6	21.8	168516	11	US-11-121-086-3
14	33.2	20.9	6432	11	US-11-043-889-3
15	31.2	19.6	5571	7	US-10-750-185-53588
16	31.2	19.6	5571	7	US-10-750-623-53588
17	31.2	19.6	15057	11	US-11-124-367A-5010
18	31.2	19.6	16139	11	US-11-124-367A-5015
19	30.4	19.1	155515	11	US-11-112-908-42
20	30.4	19.1	159660	11	US-11-112-908-43
21	30.4	19.1	177623	11	US-11-112-908-41

c	22	29.6	18.6	1178	11	US-11-112-908-479	Sequence 479, App
	23	29	18.2	34554	6	US-10-893-483-49	Sequence 49, Appl
	24	28.8	18.1	3903	11	US-11-177-000-1	Sequence 1, Appl
c	25	28.2	17.7	600	7	US-10-750-185-21614	Sequence 21614, A
	26	28.2	17.7	600	7	US-10-750-623-21614	Sequence 21614, A
c	27	28.2	17.7	1467	7	US-10-750-185-60794	Sequence 60794, A
c	28	28.2	17.7	1467	7	US-10-750-623-60794	Sequence 60794, A
c	29	28.2	17.7	611587	11	US-11-117-187-209	Sequence 209, App
	30	28	17.6	471	11	US-11-112-908-426	Sequence 426, App
c	31	28	17.6	2038	11	US-11-000-463-601	Sequence 601, App
c	32	28	17.6	2412	11	US-11-000-463-129	Sequence 129, App
	33	28	17.6	40000	7	US-10-995-561-13509	Sequence 13509, A
c	34	28	17.6	100000	11	US-11-124-368A-2899	Sequence 2899, Ap
c	35	28	17.6	149419	11	US-11-112-908-49	Sequence 49, Appl
c	36	28	17.6	161726	11	US-11-112-908-48	Sequence 48, Appl
c	37	28	17.6	161726	11	US-11-112-908-52	Sequence 52, Appl
c	38	28	17.6	166111	11	US-11-112-908-47	Sequence 47, Appl
	39	28	17.6	177623	11	US-11-112-908-41	Sequence 41, Appl
c	40	27.8	17.5	67467	11	US-11-124-368A-2889	Sequence 2889, Ap
	41	27.8	17.5	150038	11	US-11-121-086-23	Sequence 23, Appl
c	42	27.4	17.2	201	7	US-10-995-561-49253	Sequence 49253, A
c	43	27.4	17.2	201	7	US-10-995-561-49333	Sequence 49333, A
	44	27.4	17.2	201	11	US-11-124-368A-13339	Sequence 13339, A
	45	27.4	17.2	201	11	US-11-124-368A-13502	Sequence 13502, A

ALIGNMENTS

RESULT 1

US-10-995-561-3388  
; Sequence 3388, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3388  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-995-561-3388

Query Match 90.2%; Score 143.4; DB 7; Length 201;  
Best Local Similarity 97.5%; Pred. No. 3.5e-33;  
Matches 155; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy	1	TTAATGACACGACCGGCGTCCCTGCTGTGACGCTCTGGCGCTCCCTTCAGGGCTCCC	60
Db	27	TTAATGACACGACCGAC-GGCGTCCCTGCTGTGAGCTCTGGCGCTCCCTTCAGGGCTCCC	85
Qy	61	GAGCCACACGCTGGGCGCTGCTGGCTGAGGAAACATGTCATGTCCTCAGCTGAGGTG	120
Db	86	GAGCCACACGCTGGGCGTGGCTGCTGGCTGAGGAAACATGTCATGTCCTCAGCTGAGGTG	145
Qy	121	CTGC	159
Db	146	CTGC	184

RESULT 2

US-10-995-561-3411  
; Sequence 3411, A  
; Publication No. 1  
; GENERAL INFORMAT  
; APPLICANT: CARG  
; TITLE OF INVENT

TED WITH

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2006, 23:04:12 ; Search time 9938.59 Seconds  
(without alignments)  
16546.426 Million cell updates/sec

Title: US-09-846-456A-3

Perfect score: 2893

Sequence: 1 acaggcatgtggcaggtg.....ctagtcggcgcaaaacccc 2893

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_in:\*

3: gb\_env:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pt:\*

9: gb\_ro:\*

10: gb\_sts:\*

11: gb\_sy:\*

12: gb\_un:\*

13: gb\_vl:\*

14: gb\_btg:\*

15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2893	100.0	2893	6	AX351031	Sequence
2	2893	100.0	2231	6	AX351029	Sequence
3	2790.2	96.4	183999	6	AX025889	Sequence
C 4	2783.6	96.2	96717	8	AL359182	Human DNA
5	2618.8	90.5	201144	8	AF287262	Homo sapi
C 6	1973.6	68.2	183930	14	AC160520	Papio ham
7	1878	64.9	200920	14	AC161030	Colobus g
8	1435	49.6	149034	8	AF275948	Homo sapi
9	1394.4	48.2	1643	6	AF607251	Sequence
10	1394.4	48.2	1643	6	ARG28826	Sequence
11	1394.4	48.2	1643	6	AX060715	Sequence
12	1394.4	48.2	1643	6	AX060894	Sequence
C 13	1393.8	48.2	183118	14	AC160722	Aotus nan
C 14	1332.4	46.1	206547	14	AC161097	Callitru
15	1317.6	45.5	198224	14	AC161090	Callitru
16	1027.8	35.5	1197	6	AR575615	Sequence
17	1010.4	34.9	248297	14	AC160525	Saimiri b
18	889.8	30.8	175064	14	AC012230	Homo sapi

19	889.4	30.7	1167	8	AF258623	Homo sapi
20	889.4	30.7	1167	8	HA252201	Homo sapi
21	612.2	21.2	900	6	CQ769943	Sequence
22	612.2	21.2	900	6	CQ769944	Sequence
23	612.2	21.2	900	6	CQ786993	Sequence
24	612.2	21.2	900	6	CQ786994	Sequence
C 25	553.8	19.1	175064	14	AC012230	Homo sapi
26	478.8	16.6	90698	14	AC021345	Homo sapi
27	414	14.3	69570	14	AC021246	Homo sapi
C 28	377.6	13.1	166049	8	AC090947	Homo sapi
C 29	377.6	13.1	185608	8	AC027126	Homo sapi
C 30	377	13.0	164888	14	AC024101	Homo sapi
C 31	356.4	12.3	162268	8	AC146385	Pan trogl
C 32	356	12.3	81117	8	AC016898	Homo sapi
33	353.8	12.2	175999	14	AC021154	Homo sapi
34	352.2	12.2	167787	8	AC010624	Homo sapi
C 35	351.6	12.2	166743	8	AP003357	Homo sapi
36	351.6	12.2	181953	14	AC087826	Homo sapi
C 37	350.4	12.1	99593	8	HSJ857M17	Human DNA
C 38	349.4	12.1	184640	8	AC009690	Homo sapi
C 39	349.2	12.1	163218	8	AC005837	Homo sapi
40	348	12.0	206231	8	AL592309	Human DNA
C 41	347.8	12.0	159110	8	AL355296	Human DNA
C 42	347.8	12.0	183960	8	AC013445	Homo sapi
C 43	347.4	12.0	141762	8	HS198C21	Human DNA
C 44	347.2	12.0	173375	14	AC044815	Homo sapi
45	346.8	12.0	53962	8	AC009246	Homo sapi

#### ALIGNMENTS

RESULT 1  
AX351031  
LOCUS AX351031 2893 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 3 from Patent WO0183746.  
ACCESSION AX351031  
VERSION AX351031.1 GI:18616387  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1  
AUTHORS Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Deneffe, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.  
TITLE Regulatory nucleic acid sequences of the abcl gene  
JOURNAL Patent: WO 0183746-A 3 08-NOV-2001;  
Aventis Pharma S.A. (FR)  
FEATURES  
source Location/Qualifiers  
1..2893  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 100.0%; Score 2893; DB 6; Length 2893;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ACAGGGCATGTCGACGGTGCCTGTATCTCAGTTACTCGGAGGTGGAGGTGCAATGA 60  
Db 1 ACAGGGCATGTCGACGGTGCCTGTATCTCAGTTACTCGGAGGTGGAGGTGCAATGA 60  
Qy 61 GCCCAGATCGCACCATTCGACTCCAGCTGGGCAACAAAGGTGAAACTCCATCTCAATT 120  
Db 61 GCCCAGATCGCACCATTCGACTCCAGCTGGGCAACAAAGGTGAAACTCCATCTCAATT 120  
Qy 121 AAAAAAAGAAATGATTTTGGTTCGATTTCAATAGGTAGGAGAGAGAGAGAGG 180  
Db 121 AAAAAAAGAAATGATTTTGGTTCGATTTCAATAGGTAGGAGAGAGAGAGAGG 180

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2006, 17:12:15 ; Search time 1200.33 Seconds  
(without alignments)  
16062.998 Million cell updates/sec

Title: US-09-846-456A-3

Perfect score: 2893

Sequence: 1 acaggcgtatgtgagcagtg.....ctagtcggcgaataacccc 2893

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 21:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2893	100.0	2893	6	ABN99232 Human ABC
2	2893	100.0	2910	6	AAD37267 Human ABC
3	2893	100.0	3231	6	AAD37265 Human ABC
4	2893	100.0	3231	6	ABL58147 Human ABC
5	2891.4	99.9	2893	6	ABN993356 Polymorph
6	2891.4	99.9	2893	6	ABN993356 Polymorph
7	2891.4	99.9	2893	6	ABN993354 Polymorph
8	2891.4	99.9	2893	6	ABN993340 Polymorph
9	2891.4	99.9	2893	6	ABN993345 Polymorph
10	2891.4	99.9	2893	6	ABN993347 Polymorph
11	2891.4	99.9	2893	6	ABN993336 Polymorph
12	2891.4	99.9	2893	6	ABN993339 Polymorph
13	2891.4	99.9	2893	6	ABN993352 Polymorph
14	2891.4	99.9	2893	6	ABN993341 Polymorph
15	2891.4	99.9	2893	6	ABN993348 Polymorph
16	2891.4	99.9	2893	6	ABN993357 Polymorph
17	2891.4	99.9	2893	6	ABN993344 Polymorph
18	2891.4	99.9	2893	6	ABN993351 Polymorph
19	2891.4	99.9	2893	6	ABN993353 Polymorph

20 2891.4 99.9 2893 6 ABN993343 Polymorph  
21 2881 99.6 2895 6 ABN993346 Polymorph  
22 2875 99.4 2889 6 ABN993349 Polymorph  
23 2873 99.3 2888 6 ABN993355 Polymorph  
24 2873 99.3 2903 6 ABN993337 Polymorph  
25 2865 99.0 2884 6 ABN993350 Polymorph  
26 2790.2 96.4 183999 4 AAF92831 Human ABC  
27 2790.2 96.4 183999 13 ADU76470 Human ABC  
28 2793.6 96.2 21000 13 ADU77194 Type II.d  
29 2411.4 83.4 2893 6 ABN993338 Polymorph  
30 1435 49.6 149034 11 ADP65433 Human ABC  
31 1394.4 48.2 1643 4 AAF24681 Nucleotid  
32 1394.4 48.2 1643 4 AAF24703 Nucleotid  
33 1027.8 35.5 1197 6 ABL58400 Human lar  
34 899.4 30.7 1033 8 ACC49024 ABC1 gene  
35 857.8 29.7 1115 8 ACC49021 ABC1 gene  
36 612.2 21.2 900 12 ADJ77896 Phenotype  
37 612.2 21.2 900 12 ADJ77895 Phenotype  
38 377.6 13.1 166043 12 ADL08127 Human gen  
39 350.4 12.1 79544 12 ADQ97764 Human can  
40 336.4 11.6 151909 14 AEB96535 Human CAB  
41 333 11.5 80928 12 ADO25290 Human pro  
42 330.8 11.4 20645 4 AAL05355 Human rep  
43 330.8 11.4 20645 4 ABL98224 Human tes  
44 330.6 11.4 5076 5 ABA16699 Human ner  
45 328.8 11.4 118788 12 ADP80536 Human HPC

#### ALIGNMENTS

#### RESULT 1

ABN99232  
ID ABN99232 standard; DNA; 2893 BP.  
XX  
AC ABN99232;  
XX  
DT 17-JAN-2003 (first entry)  
XX  
DE Human ABCA1 transporter gene promoter.  
XX  
KW Human; ABCA1; transporter; ATP-binding cassette;  
KW high density lipoprotein; HDL; cholesterol; familial HDL deficiency;  
KW Tangier disease; myocardial infarction; atherosclerosis;  
KW cardiovascular disease; promoter; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200236770-A2.  
XX  
PD 10-MAY-2002.  
XX  
PF 12-OCT-2001; 2001WO-FR003182.  
XX  
PR 31-OCT-2000; 2000FR-00014037.  
XX  
PR 11-DEC-2000; 2000US-0254108P.  
XX  
PA (AVET ) AVENTIS PHARMA SA.  
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
XX  
PI Deneffle P, Rosier M, Arnould-Reguigne I, Duverger N, Cambien F;  
XX WPI; 2002-435691/46.  
XX  
XX New polymorphisms in the human ABCA1 gene, useful for diagnosing  
PT predisposition to myocardial infarct and other cardiovascular diseases.  
XX  
PS Claim 4; Page 109; 297pp; French.  
XX  
XX The present sequence is the human ATP-binding cassette (ABCA1)  
CC transporter gene promoter. This sequence can be used for diagnosing  
CC (predisposition to) diseases associated with the plasma level of high  
CC density lipoprotein (HDL) cholesterol, especially familial HDL deficiency



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OM nucleic - nucleic search, using sw model

Run on: February 9, 2006, 15:01:42 ; Search time 8084.71 Seconds  
(without alignments)  
16742.090 Million cell updates/sec

Title: US-09-846-456A-3

Perfect score: 2893

Sequence: 1 acagggcatggtggcagggtg.....ctagtcgccgcaaaacccc 2893

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_est3.\*
- 4: gb\_est4.\*
- 5: gb\_est5.\*
- 6: gb\_est6.\*
- 7: gb\_est7.\*
- 8: gb\_est8.\*
- 9: gb\_est9.\*
- 10: gb\_est10.\*
- 11: gb\_est11.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	324	11.2	3004	CR857583	CR857583 Pongo pyg
2	322.2	11.1	3004	CR857583	CR857583 Pongo pyg
3	285.4	9.9	3127	CR860188	CR860188 Pongo pyg
4	275.6	9.5	4503	CR858665	CR858665 Pongo pyg
C 5	267	9.2	1122	AY927481	AY927481 Homo sapi
C 6	247.6	8.6	2127	CR860188	CR860188 Pongo pyg
7	247.2	8.5	3178	AL832411	AL832411 Homo sapi
C 8	239.6	8.3	4503	CR858665	CR858665 Pongo pyg
C 9	237.8	8.2	289	AW748338	AW748338 RC6-BT025
C 10	234.4	8.1	1741	CR603303	CR603303 full-length
C 11	233	8.1	770	BZ612146	BZ612146 WHACL55TF
C 12	231.2	8.0	1047	EX380958	EX380958
C 13	221.2	7.6	457	AW816516	AW816516 QVO-ST023
14	220.6	7.6	696	BU616112	BU616112 UI-H-DF0
C 15	220.2	7.6	5920	CR936634	CR936634 Homo sapi
C 16	219.4	7.6	577	CR936634	CR936634 Homo sapi
17	218.6	7.6	544	AQ265389	AQ265389 CITBI-E1
18	217.8	7.5	2403	BC035389	BC035389 Homo sapi
19	217	7.5	350	CN268016	CN268016 170005318
20	217	7.5	620	BQ775487	BQ775487 UI-H-FH0
21	216.4	7.5	990	BM803650	BM803650 AGENCOURT
22	216.2	7.5	467	BU735183	BU735183 UI-B-DW0

23	215.4	7.4	897	5	BU52764	AGENCOURT
C 24	215.2	7.4	719	9	AQ475181	CITBI-E1
25	215.2	7.4	1686	4	CR619941	full-length
26	215.2	7.4	1755	4	CR609780	full-length
C 27	215.2	7.4	2472	4	HSR803556	
C 28	215.2	7.4	5941	4	CR857073	Pongo pyg
29	214.8	7.4	477	5	BU660913	cl65h02.2
30	214.8	7.4	659	5	BU660648	cl62f05.2
31	214.8	7.4	771	5	EX099350	EX099350
32	214.8	7.4	782	5	EX348886	EX348886
33	214.8	7.4	789	5	EX390419	EX390419
34	214.8	7.4	1485	4	CR610354	full-length
35	214.8	7.4	1903	4	CR619058	full-length
C 36	214.4	7.4	423	3	BM991096	BM991096 UI-H-D10
37	214.4	7.4	704	11	CR957968	CR957968 Homo sapi
C 38	214.2	7.4	581	9	AQ347610	RPCI11-12
39	214	7.4	435	5	AX472224	RKZP686P
C 40	213.4	7.4	338	1	AW023111	AW023111 df49d08.Y
41	213.4	7.4	666	10	AG075934	AG075934 Pan trogl
C 42	213.4	7.4	688	9	BZ413191	BZ413191 HSC 00387
43	213.2	7.4	493	9	B50449	B50449 CIT-HSP-422
C 44	213.2	7.4	622	9	AQ537948	AQ537948 RPCI-11-3
45	213	7.4	514	1	AI754653	AI754653 cr38c08.x

#### ALIGNMENTS

RESULT 1  
CR857583/c  
LOCUS  
DEFINITION Pongo pygmaeus mRNA; cDNA DKFZp459M1426 (from clone DKFZp459M1426).  
ACCESSION CR857583  
VERSION CR857583.1 GI:55726174  
KEYWORDS HNC.  
SOURCE Pongo pygmaeus (orangutan)  
ORGANISM

REFERENCE 1 (bases 1 to 3004)  
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.  
CONSTRM The German cDNA Consortium  
TITLE Direct Submission  
JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY  
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BWPZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseeldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp459M1426) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp459M1426  
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

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/tissue\_type="cortex"  
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166..1437  
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CDS

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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 19:02:01 ; Search time 1646.48 Seconds  
(without alignments)  
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Title: US-09-846-456A-3

Perfect score: 2893

Sequence: 1 acaggcagtggtgagcagtg.....ctagtcggcgcaaaacccc 2893

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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13	2891.4	99.9	2893	3	US-09-846-827-146
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19	2891.4	99.9	2893	3	US-09-846-827-155
20	2891.4	99.9	2893	3	US-09-846-827-157
21	2891.4	99.9	2893	3	US-09-846-827-158
22	2881	99.6	2895	3	US-09-846-827-147
23	2875	99.4	2889	3	US-09-846-827-150

24 2873 99.3 2888 3 US-09-846-827-156 Sequence 156, App  
25 2873 99.3 2903 3 US-09-846-827-138 Sequence 138, App  
26 2865 99.0 2884 3 US-09-846-827-151 Sequence 151, App  
27 2842 98.2 159138 8 US-10-719-993-6777 Sequence 6777, App  
28 2842 98.2 159138 8 US-10-741-600-17613 Sequence 17613, A  
29 2790.2 96.4 183999 7 US-10-745-377-1 Sequence 1, Appli  
30 2790.2 96.4 183999 8 US-10-872-113-1 Sequence 1, Appli  
31 1435 49.6 149034 9 US-10-287-436A-956 Sequence 956, App  
32 1394.4 48.2 1643 8 US-10-920-989-3 Sequence 3, Appli  
33 1394.4 48.2 1643 9 US-10-972-836-3 Sequence 3, Appli  
34 377.6 13.1 166043 7 US-10-235-192A-46 Sequence 46, Appl  
35 330.8 11.4 20645 3 US-09-764-891-8043 Sequence 8043, Ap  
36 327 11.3 141121 8 US-10-741-600-17651 Sequence 17651, A  
37 326.6 11.3 82547 5 US-10-225-567A-675 Sequence 12, Appl  
38 326.6 11.2 53779 9 US-10-737-082-85 Sequence 85, Appl  
39 323.8 11.2 53779 9 US-10-765-790-85 Sequence 85, Appl  
40 323.8 11.2 130244 9 US-10-461-862-104 Sequence 104, App  
41 323.6 11.2 141121 8 US-10-741-600-17651 Sequence 17651, A  
42 322.6 11.1 148935 8 US-10-741-600-17708 Sequence 17708, A  
43 322 11.1 148935 8 US-10-741-600-17735 Sequence 17735, A  
44 321.8 11.1 27509 8 US-10-741-600-17735 Sequence 17735, A  
45 321.6 11.1 44063 7 US-10-322-281-718 Sequence 718, App

## ALIGNMENTS

## RESULT 1

US-09-846-456-3  
; Sequence 3, Application US/09846456

; Patent No. US20020146792A1

; GENERAL INFORMATION:

; APPLICANT: Rosier, Marie

; APPLICANT: Prades, Catherine

; APPLICANT: Lemoine, Cendrline

; APPLICANT: Naudin, Laurence

; APPLICANT: Deneffe, Patrice

; APPLICANT: Duverger, Nicolas

; APPLICANT: Brewer, Bryan

; APPLICANT: Remaley, Alan

; APPLICANT: Fojo, Silvia

; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying

; FILE REFERENCE: 3806.0505

; CURRENT APPLICATION NUMBER: US/09/846.456

; PRIOR FILING DATE: 2001-05-02

; PRIOR FILING DATE: 2000-05-02

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 2893

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-846-456-3

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 181 AGATGGAGGGTTCAGGAGATCTAATTACTCTTAAATATCATGTAGGAAAGATAACACCT 240

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OM nucleic - nucleic search, using sw model

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Title: US-09-846-456A-3  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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6	327.8	11.3	141121	7	US-10-995-561-13262
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8	322.2	11.1	141121	7	US-10-995-561-13262
9	322	11.1	148935	7	US-10-995-561-13308
10	321.8	11.1	27509	7	US-10-995-561-13319
11	321.4	11.1	100001	7	US-10-944-272-1
12	321.4	11.1	100001	11	US-11-096-191-718
13	321	11.1	79528	7	US-10-276-233A-6
14	318.8	11.0	51917	7	US-10-995-561-13338
15	317.2	11.0	161994	11	US-11-112-908-57
16	314.2	10.9	159695	11	US-11-121-086-56
17	314	10.9	135019	7	US-10-849-438-11
18	307.2	10.6	79528	7	US-10-276-233A-6
19	307.2	10.6	86081	7	US-10-995-561-13246
20	306.4	10.6	199321	11	US-11-121-086-10
21	306	10.6	86950	7	US-10-857-780-5

22	305.8	10.6	1080000	7	US-10-928-446A-1	Sequence 1, Appl
23	305.8	10.6	1080000	7	US-10-928-446A-181	Sequence 181, App
24	305.8	10.6	1080000	7	US-10-928-446A-183	Sequence 183, App
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31	305.8	10.6	1080000	7	US-10-928-446A-197	Sequence 197, App
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33	305.8	10.6	1080000	7	US-10-928-446A-201	Sequence 201, App
34	303.8	10.5	161874	11	US-11-121-086-75	Sequence 75, Appl
35	303.2	10.5	149419	11	US-11-112-908-49	Sequence 49, Appl
36	303.2	10.5	161726	11	US-11-112-908-48	Sequence 48, Appl
37	303.2	10.5	161726	11	US-11-112-908-52	Sequence 52, Appl
38	303.2	10.5	166111	11	US-11-112-908-47	Sequence 47, Appl
39	303	10.5	175023	11	US-11-121-086-18	Sequence 18, Appl
40	302.6	10.5	135019	7	US-10-849-438-11	Sequence 11, Appl
41	302.4	10.5	175416	11	US-11-121-086-43	Sequence 43, Appl
42	302	10.4	67088	7	US-10-995-561-13365	Sequence 13365, A
43	302	10.4	160226	11	US-11-121-086-29	Sequence 29, Appl
44	301.4	10.4	165857	11	US-11-121-086-34	Sequence 34, Appl
45	300.6	10.4	215308	11	US-11-121-086-77	Sequence 77, Appl

## ALIGNMENTS

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; Sequence 13230, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
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; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13230  
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; TYPE: DNA  
; ORGANISM: Homo sapiens  
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; LOCATION: (1)...(159138)  
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables  
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Db	3096	CCGGCATGGTGGCAGGTGCTGTAATCTCAGTTACTCGGAGGTGAGTTGCAATGAG	3155	
QY	62	CCAGATCGCACCATTCGACTCCAGCTGGCAACAAAGGTGAACTCCATCTCAATTA	121	
Db	3156	CCAGATCGCACCATTCGACTCCAGCTGGCAACAAAGGTGAACTCCATCTCAATTA	3215	
QY	122	AAAAAAAAGATGATTTTGGTGGTCTGACTTCAATAGGTAGGAGAGGAGAGGAGGA	181	
Db	3216	AAAAAAAAGATGATTTTGGTGGTCTGACTTCAATAGGTAGGAGAGGAGAGGAGGA	3275	
QY	182	GATGGAGGTTCAGGGAGATCTAATTAATCTCTTAAATCATGCTAGGAAGATTAACACCTT	241	
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Title: US-09-846-456A-2  
Perfect score: 357  
Sequence: 1 tggaggctcagctgagagg.....gagggaaggaagctgtgttg 357

Scoring table: IDENTITY\_NUC  
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	351.2	98.4	183999	8	US-10-872-113-1
6	341.4	95.6	159138	8	US-10-719-993-6777
7	341.4	95.6	159138	8	US-10-741-600-17613
8	340.2	95.3	10545	6	US-10-452-510-14
9	340.2	95.3	10545	7	US-10-617-334-14
10	340.2	95.3	10545	7	US-10-744-465-14
11	340.2	95.3	10545	8	US-10-833-679-14
12	340.2	95.3	10545	9	US-10-818-279-14
13	203.8	57.1	1062	3	US-09-992-600A-101
14	203.8	57.1	1062	3	US-09-924-340-101
15	203.8	57.1	1062	3	US-09-992-095B-101
16	203.8	57.1	1062	3	US-09-999-570-101
17	203.8	57.1	1062	5	US-10-000-489-101
18	203.8	57.1	1062	5	US-10-000-986-101
19	203.8	57.1	1062	6	US-10-154-678-101
20	203.8	57.1	1062	6	US-10-001-142-101
21	203.8	57.1	1062	8	US-10-838-854-101
22	186.4	52.2	201	8	US-10-719-993-10219
23	186.4	52.2	201	8	US-10-741-600-27292

ALIGNMENTS

RESULT 1  
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; Sequence 2, Application US/09846456  
; Patent No. US20020146792A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosier, Marie  
; APPLICANT: Prades, Catherine  
; APPLICANT: Lemoine, Cendrine  
; APPLICANT: Naudin, Laurent  
; APPLICANT: Denefle, Patrice  
; APPLICANT: Duverger, Nicolas  
; APPLICANT: Brewer, Bryan  
; APPLICANT: Remaley, Alan  
; APPLICANT: Fojo, Silvia  
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying  
; FILE REFERENCE: 3806.0505  
; CURRENT APPLICATION NUMBER: US/09/846,456  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/201,280  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 357  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-846-456-2

Query Match 100.0%; Score 357; DB 3; Length 357;  
Best Local Similarity 100.0%; Pred. No. 3.9e-105; Indels 0; Gaps 0;  
Matches 357; Conservative 0; Mismatches 0

Qy	1	TGGAGGCTCTCAGCTGAGAGGGCTGGATTAGCAGTCCTCATTTGGTGTATGGCTTTGCAGCA	60
Db	1	TGGAGGCTCTCAGCTGAGAGGGCTGGATTAGCAGTCCTCATTTGGTGTATGGCTTTGCAGCA	60
Qy	61	ATAACTGATGGCTGTTTCCCTCTCTCTTATCTTTTCAGTTATGACACGACGGCGGT	120
Db	61	ATAACTGATGGCTGTTTCCCTCTCTCTTATCTTTTCAGTTATGACACGACGGCGGT	120
Qy	121	CCCTGCTGTCAGCTGCGGCTGCGCTTCCAGGGTCCCGACGACACGCTGGCGGTCT	180
Db	121	CCCTGCTGTCAGCTGCGGCTGCGCTTCCAGGGTCCCGACGACACGCTGGCGGTCT	180
Qy	181	GGCTGAGGGAACATGGCATGTTGGCCCTCAGCTAGGTTGCTGTGTGGAAGAACCTCACT	240

GenCore version 5.1.7  
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(without alignments)  
16062.998 Million cell updates/sec

Title: US-09-846-456A-2

Perfect score: 357

Sequence: 1 tggaggctcagctgagagg.....gaggggaaggagctgtgttg 357

Scoring table: IDENTITY NUC

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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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14: geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	357	100.0	357	6	AAD37266 Human ABC
2	357	100.0	357	6	ABL58148 Human ABC
3	353.8	99.1	149034	11	ADP65433 Human ABC
4	351.2	98.4	183999	4	AAF92831 Human ABC
5	351.2	98.4	183999	13	ADU76470 Human ABC
6	340.2	95.3	10545	3	AAC69132 Human ABC
7	203.8	57.1	1062	8	ACC51110 Human ABC
8	159.4	44.6	10442	4	AAF24680 Nucleotid
9	159.4	44.6	10442	4	AAF24702 Nucleotid
10	159.4	44.6	10442	13	ADP23549 PRO polyp
11	159.4	44.6	10442	14	ADY15089 DNA encod
12	159.4	44.6	10442	14	AEA23717 Human PRO
13	159.4	44.6	10474	4	AAF24685 Nucleotid
14	159.4	44.6	10474	4	AAF24686 Nucleotid
15	159.4	44.6	10474	4	AAF24708 Nucleotid
16	159.4	44.6	10474	4	AAF24707 Nucleotid
17	159	44.5	159	6	AAD37269 Human ABC
18	158.4	44.4	10381	10	ADD94069 Human ATP
19	158.4	44.4	10423	10	ADD94070 Human ATP

20	157.4	44.1	159	6	ABN99235
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22	147	41.2	158	6	ABN99234
23	147	41.2	1402	13	ADQ38534
24	147	41.2	1859	13	ADQ38532
25	147	41.2	10405	13	ADQ38535
26	146.4	41.0	201	13	ADQ44142
27	146.4	41.0	201	13	ADQ44225
28	146.4	41.0	201	13	ADQ44200
29	145.8	40.8	446	4	AAS04035
30	145.8	40.8	7086	4	ABA09200
31	145.8	40.8	7086	4	AAK52667
32	145.8	40.8	7260	4	AAI70315
33	145.8	40.8	7260	4	AAD21326
34	145.8	40.8	7281	4	AAK51683
35	145.8	40.8	9741	4	AAS06120
36	145.8	40.8	9741	6	ABL37273
37	145.8	40.8	9741	6	ABL58146
38	145.8	40.8	9854	4	AAS06121
39	145.8	40.8	9870	6	ABN99307
40	145.8	40.8	9870	6	ABN99302
41	145.8	40.8	9870	6	ABN99305
42	145.8	40.8	9870	6	ABN99317
43	145.8	40.8	9870	6	ABN99321
44	145.8	40.8	9870	6	ABN99323
45	145.8	40.8	9870	6	ABN99309

#### ALIGNMENTS

##### RESULT 1

AAD37266  
ID AAD37266 standard; DNA; 357 BP.

XX  
AC AAD37266;

XX  
DT 21-AUG-2002 (first entry)

XX  
DE Human ABC1 transcription regulatory DNA #2.

XX  
KW Human; ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis; cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.

XX  
OS Homo sapiens.

XX  
FN WO200183746-A2.

XX  
PD 08-NOV-2001.

XX  
PF 02-MAY-2001; 2001WO-EP005488.

XX  
PR 02-MAY-2000; 2000US-0201280P.

XX  
PA (AVET ) AVENTIS PHARMA SA.

XX  
PI Rosier-Montus M, Prades C, Lemoine C, Naudin L, Deneffe P;

XX  
PI Brewer B, Duverger N, Remaley A, Santamarina-Fojo S;

XX  
DR WPI; 2002-154404/20.

XX  
FT Isolated nucleic acid useful for modifying the ATP-binding cassette 1 (ABC1) and screening for candidate modulatory compounds or substances.

XX  
PS Claim 2; Page 131; 152pp; English.

XX  
CC The invention relates a nucleic acid which is capable of regulating the transcription of human ATP-binding cassette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholesterol metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABC1 gene. They are used in antisense therapy. Compositions comprising sequences of the

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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 22:47:42 ; Search time 94.8953 Seconds  
(without alignments)  
3382.690 Million cell updates/sec

Title: US-09-846-456A-2

Perfect score: 357

Sequence: 1 tggaggctcagctgagagg.....gaggggaaggaagctgtgttg 357

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	186.4	52.2	201	7	US-10-995-561-23954
3	155.6	43.6	201	7	US-10-995-561-24507
4	147	41.2	1402	7	US-10-995-561-85
5	147	41.2	1859	7	US-10-995-561-84
6	147	41.0	10405	7	US-10-995-561-83
7	146.4	41.0	201	7	US-10-995-561-3388
8	146.4	41.0	201	7	US-10-995-561-3411
9	146.4	41.0	201	7	US-10-995-561-3429
10	145.8	40.8	10412	11	US-11-085-309A-7
11	65	18.2	6786	11	US-11-085-309A-8
12	56	15.7	201	7	US-10-995-561-24209
13	44	12.3	201	7	US-10-995-561-24210
14	37.8	10.6	168516	11	US-11-121-086-3
15	34.6	9.7	6768	11	US-11-043-889-1
16	33.6	9.4	600	11	US-11-136-527-7810
17	33.6	9.4	2432	11	US-11-136-527-3714
18	33.4	9.4	1598	7	US-10-750-185-32881
19	33.4	9.4	1598	7	US-10-750-623-32881
20	33.2	9.3	6432	11	US-11-043-889-3
21	33	9.2	18238	7	US-10-995-561-13386

C 22	32.4	9.1	1775	11	US-11-136-527-123	Sequence 123, Appl
C 23	32.4	9.1	155515	11	US-11-112-908-42	Sequence 42, Appl
C 24	32.4	9.1	159660	11	US-11-112-908-43	Sequence 43, Appl
C 25	32.4	9.1	177623	11	US-11-112-908-41	Sequence 41, Appl
C 26	32	9.0	3332	11	US-11-136-527-74	Sequence 74, Appl
C 27	31.8	8.9	171423	11	US-11-121-086-85	Sequence 85, Appl
C 28	31.2	8.7	5571	7	US-10-750-185-53588	Sequence 53588, A
C 29	31.2	8.7	5571	7	US-10-750-623-53588	Sequence 53588, A
C 30	31.2	8.7	15057	11	US-11-124-367A-5015	Sequence 5015, Ap
C 31	31.2	8.7	16139	11	US-11-124-367A-5010	Sequence 5010, Ap
C 32	30.6	8.6	600	11	US-11-136-527-6738	Sequence 6738, Ap
C 33	30.6	8.6	1860	11	US-11-136-527-2642	Sequence 2642, Ap
C 34	30.4	8.5	28536	11	US-11-011-332A-152	Sequence 152, App
C 35	30.4	8.5	100000	11	US-11-124-368A-2899	Sequence 2899, Ap
C 36	30.4	8.5	149382	7	US-10-995-561-13272	Sequence 13272, A
C 37	30.2	8.5	201	7	US-10-995-561-132457	Sequence 32457, A
C 38	30.2	8.5	956	7	US-10-750-185-56717	Sequence 56717, A
C 39	30.2	8.5	956	7	US-10-750-623-56717	Sequence 56717, A
C 40	30.2	8.5	57917	7	US-10-995-561-13299	Sequence 13299, A
C 41	30.2	8.5	387780	7	US-10-995-561-13259	Sequence 13259, A
C 42	30	8.4	120697	11	US-11-121-086-48	Sequence 48, Appl
C 43	29.8	8.3	177175	11	US-11-121-086-78	Sequence 78, Appl
C 44	29.8	8.3	189993	11	US-11-121-086-78	Sequence 78, Appl
C 45	29.8	8.3	199130	7	US-10-995-561-13233	Sequence 13233, A

ALIGNMENTS

RESULT 1

US-10-995-561-13230  
; Sequence 13230, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13230  
; LENGTH: 159138  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(159138)  
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables  
US-10-995-561-13230

Query Match	95.5%	Score 341;	DB 7;	Length 159138;
Best Local Similarity	98.6%	Pred. No. 1.1e-89;		
Matches 352;	Conservative 2;	Mismatches 1;	Gaps 1;	
Qy	1	TGGAGGCTCAGCTGAGAGGCTGGATTAGCAGTCCTCATTTGGTGTATGGCTTTGCAGCA	60	
Db	30284	TGGAGGCTCAGCTGAGAGGCTGGATTAGCAGTCCTCATTTGGTGTATGGCTTTGCAGCA	30343	
Qy	61	ATACTGATGGCTGTTTCCCTCCTCTCTTATCTTTTCACTTAATGACGACCGGGCGT	120	
Db	30344	ATACTGATGGCTGTTTCCCTCCTCTCTTATCTTTTCACTTAATGACGACCGAC	30402	
Qy	121	CCCTGCTGTCAGCTCTGGCGCTGCTTCCAGGGCTCCGAGCCACACGCTGGGGTCT	180	
Db	30403	CCCTGCTGTCAGCTCTGGCGCTGCTTCCAGGGCTCCGAGCCACACGCTGGGGTCT	30462	
Qy	181	GGCTGAGGACATGGCATGTTGGCTTGGCTGAGTGTGCTGCTGGAAGAACTCACT	240	
Db	30463	GGCTGAGGACATGGCTTGTGCTGCTGAGTGTGCTGCTGGAAGAACTCACT	30522	

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Title: US-09-846-456A-2

Perfect score: 357

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Scoring table: IDENTITY NUC

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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: gb\_om.\*

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6: gb\_pat.\*

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9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vl.\*

14: gb\_btg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	340.2	95.3	480	8	HGA252277	Sequence
5	340.2	95.3	10545	6	AR393492	Sequence
6	340.2	95.3	129608	8	AL353685	Human DNA
7	340.2	95.3	175064	14	AC012230	Homo sapi
8	340.2	95.3	201144	8	AP287262	Homo sapi
9	294.2	82.4	183930	14	AC160520	Papio ham
10	294.2	82.4	207933	14	AC160521	Papio ham
11	292.6	82.0	200920	14	AC161030	Colobus g
12	285	79.8	183118	14	AC160722	Aotus nan
13	284	79.6	171939	14	AC160721	Aotus nan
14	280.8	78.7	198224	14	AC161090	Callithri
15	280.8	78.7	208547	14	AC161097	Callicebu
16	271.4	76.0	248297	14	AC160525	Saimiri b
17	251.2	70.4	90698	14	AC021345	Homo sapi
18	231	64.7	179848	14	AC139880	Lemur cat

19	203.8	57.1	1062	6	AR583753	Sequence
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23	203.4	57.0	447	6	AX983086	Sequence
24	184.2	51.6	200	8	AF258623S2	Homo sapi
25	159.4	44.6	10442	6	CS031389	Sequence
26	159.4	44.6	10442	6	CS040341	Sequence
27	159.4	44.6	10442	6	CS108251	Sequence
28	159.4	44.6	10442	6	AR607250	Sequence
29	159.4	44.6	10442	6	AR628825	Sequence
30	159.4	44.6	10442	6	AX060713	Sequence
31	159.4	44.6	10442	6	AX060892	Sequence
32	159.4	44.6	10442	8	AF285167	Homo sapi
33	159.4	44.6	10474	6	AR607255	Sequence
34	159.4	44.6	10474	6	AR607256	Sequence
35	159.4	44.6	10474	6	AR628830	Sequence
36	159.4	44.6	10474	6	AR628831	Sequence
37	159.4	44.6	10474	6	AX060719	Sequence
38	159.4	44.6	10474	6	AX060721	Sequence
39	159.4	44.6	10474	6	AX060898	Sequence
40	159.4	44.6	10474	6	AX060900	Sequence
41	159	44.5	159	6	AX351033	Sequence
42	147	41.2	697	8	AF258627	Homo sapi
43	145.8	40.8	446	6	AX127764	Sequence
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#### ALIGNMENTS

RESULT 1  
AX351030  
LOCUS AX351030 357 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 2 from Patent WO0183746.  
ACCESSION AX351030  
VERSION AX351030.1 GI:18616386

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
1 Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P.,  
Brewer, B., Duverger, N., Remaley, A. and Santamarina-Pojo, S.  
Regulatory nucleic acid sequences of the abcl gene  
Patent: WO 0183746-A 2 08-NOV-2001;  
Aventis Pharma S.A. (FR)

TITLE  
JOURNAL  
FEATURES  
Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.8e-94;  
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Db 1 TGGAGGTTCTCAGCTGAGAGGCTGGATTAGCAGTCCTCATTTGGTGTATGGCTTTGACGA 60

QY 61 ATAACTGATGGCTGTTTCCCTCTCTGCTTTATCTTTTACGTAGTTAATGACACGACACGGGGT 120

Db 61 ATAACTGATGGCTGTTTCCCTCTCTGCTTTATCTTTTACGTAGTTAATGACACGACACGGGGT 120

QY 121 CCCTGCTGTGAGCTGTGGCGCTCCGCTCCAGGGCTCCGAGCCACACGCTGGGGCTCT 180

Db 121 CCCTGCTGTGAGCTGTGGCGCTCCGCTCCAGGGCTCCGAGCCACACGCTGGGGCTCT 180

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OM nucleic - nucleic search, using sw model

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Title: US-09-846-456A-2

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Post-processing: Minimum Match 0%

Maximum Match 100%

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7: gb\_est7.\*

8: gb\_est8.\*

9: gb\_est9.\*

10: gb\_est10.\*

11: gb\_est11.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	159.4	44.6	595	3	BP280045 BP280045
5	145.8	40.8	583	3	BP200657 BP200657
6	145.8	40.8	663	5	BX555241 DKF2p781F
7	145.2	40.7	583	3	BP287529 BP287529
8	144.2	40.4	736	1	AU135588 AU135588
9	75.8	21.2	619	2	BB657864 BB657864
10	75.8	21.2	478	4	AK051920 Mus muscu
				8	Z44377 HSC12B081 n
				2	BG384217 303216 MA
				8	DN853427 419571 B
				4	CNS0EXBH
				3	BJ901916 BJ901916
				8	CX260141 1313535 N
				5	BX311478 BX311478
				7	CO27141 AGENCOURT
				5	BY175500 BY175500
				8	DN485045 M102C08.3
				10	CNS02DO1
				5	BU867612 M102C08 P

23	40.8	11.4	442	8	DN494513
24	40.2	11.3	888	6	CB209313
25	39.8	11.1	696	7	CO358299
26	39.6	11.1	910	10	CNS0060N
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44	37	10.4	623	5	BM343397
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## ALIGNMENTS

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LOCUS CH240\_259B12.TJ CHORI-240 Bos taurus genomic clone CH240\_259B12, linear GSS 18-MAR-2003  
DEFINITION genomic survey sequence.  
ACCESSION BZ865821  
VERSION BZ865821.1 GI:29093226  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 648)  
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Teagay,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Chen,D., Riggs,F., de Jong,P., Crawford,A.M. and McEwan,J.C.  
TITLE Bovine BAC End Sequences from Library CHORI-240  
JOURNAL Unpublished (2003)  
COMMENT Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering\_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by AgResearch Ltd., New Zealand and The Institute of Genomic Research (TIGR), USA.  
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Location/Qualifiers  
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(without alignments)  
16742.090 Million cell updates/sec

Title: US-09-846-456A-1  
Perfect score: 3231  
Sequence: 1 acaggcatgtgaggtg.....gccccacatccccaccactt 3231

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_ges1:\*  
10: gb\_ges2:\*  
11: gb\_ges3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	336	10.4	763	1	AU121731	AU121731
C 2	324	10.0	3004	4	CR857583	Pongo pyg
3	322.2	10.0	3004	4	CR857583	Pongo pyg
4	314.4	9.7	663	5	EX955241	DKFZp781F
5	285.4	8.8	3127	4	CR860188	Pongo pyg
6	275.6	8.5	4503	4	CR858665	Pongo pyg
C 7	267	8.3	1122	4	AY927481	Homo sapi
C 8	247.6	7.7	3127	4	CR860188	Pongo pyg
C 9	247.2	7.7	3178	4	HSM803719	AL832411 Homo sapi
C 10	239.6	7.4	4503	4	CR858665	Pongo pyg
C 11	237.8	7.4	289	1	AW748338	AW748338 RC6-BT025
C 12	234.4	7.3	1741	4	CR603303	full-length
C 13	233	7.2	770	9	BZ612146	WHACL55TF
C 14	231.2	7.2	1047	5	EX380958	BR380958
C 15	223.4	6.9	583	3	BP287529	BP287529
16	221.8	6.9	736	1	AU135588	AU135588
17	221.4	6.9	583	3	BP200657	BP200657
18	221.4	6.9	583	3	BP280727	BP280727
19	221.4	6.9	595	3	BP280045	BP280045
C 20	221.2	6.8	457	1	AW816516	AW816516 QVO-ST023
21	220.6	6.8	696	5	BU616112	UI-H-D90-
C 22	220.2	6.8	5920	4	CR936634	Homo sapi

## ALIGNMENTS

RESULT 1  
AU121731  
LOCUS AU121731 MAMMAL Homo sapiens cDNA clone MAMMAL000851 5', mRNA linear EST 01-AUG-2002  
DEFINITION AU121731 MAMMAL Homo sapiens cDNA clone MAMMAL000851 5', mRNA linear EST 01-AUG-2002  
ACCESSION AU121731  
VERSION AU121731.1 GI:10936966  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 763)  
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.  
HRI human cDNA project  
Unpublished (2000)  
Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: genomics@hri.co.jp  
HRI human cDNA project; 5' & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  
Location/Qualifiers  
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/clone="MAMMAL000851"  
/tissue\_type="mammary gland"  
/clone\_lib="MAMMAL"  
/note="Vector: pME18SFL3"

Query Match 10.4%; Score 336; DB 1; Length 763;  
Best Local Similarity 100.0%; Pred. No. 7e-23;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2006, 17:12:15 ; Search time 1340.57 Seconds  
(without alignments)  
16062.998 Million cell updates/sec

Title: US-09-846-456A-1

Perfect score: 3231

Sequence: 1 acaggcgatggtggcagggtg.....gccccacatcccccaccactt 3231

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: geneseqn2000s.\*
- 4: geneseqn2001as.\*
- 5: geneseqn2001bs.\*
- 6: geneseqn2002as.\*
- 7: geneseqn2002bs.\*
- 8: geneseqn2003as.\*
- 9: geneseqn2003bs.\*
- 10: geneseqn2003cs.\*
- 11: geneseqn2003ds.\*
- 12: geneseqn2004as.\*
- 13: geneseqn2004bs.\*
- 14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3231	100.0	3231	6	AAD37265 Human ABC
2	3231	100.0	3231	6	ABL58147 Human ABC
3	3127.8	96.8	183999	4	Aaf92831 Human ABC
4	3127.8	96.8	183999	13	ADU76470 Human ABC
5	3121.6	96.6	21000	13	ADT77194 Type II d
6	2910	90.1	2910	6	AAD37267 Human ABC
7	2893	89.5	2893	6	ABN99332 Human ABC
8	2891.4	89.5	2893	6	ABN99356 Polymorph
9	2891.4	89.5	2893	6	ABN99342 Polymorph
10	2891.4	89.5	2893	6	ABN99354 Polymorph
11	2891.4	89.5	2893	6	ABN99340 Polymorph
12	2891.4	89.5	2893	6	ABN99345 Polymorph
13	2891.4	89.5	2893	6	ABN99347 Polymorph
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15	2891.4	89.5	2893	6	ABN99339 Polymorph
16	2891.4	89.5	2893	6	ABN99352 Polymorph
17	2891.4	89.5	2893	6	ABN99341 Polymorph
18	2891.4	89.5	2893	6	ABN99348 Polymorph
19	2891.4	89.5	2893	6	ABN99357 Polymorph

20	2891.4	89.5	2893	6	ABN99344
21	2891.4	89.5	2893	6	ABN99351
22	2891.4	89.5	2893	6	ABN99353
23	2891.4	89.5	2893	6	ABN99343
24	2881	89.2	2895	6	ABN99346
25	2875	89.0	2889	6	ABN99349
26	2873	88.9	2888	6	ABN99355
27	2873	88.9	2903	6	ABN99337
28	2865	88.7	2884	6	ABN99350
29	2411.4	74.6	2893	6	ABN99338
30	1773	54.9	149034	11	ADP65433
31	1485.4	46.0	1643	4	AAF24681
32	1485.4	46.0	1643	4	AAF24703
33	1134.8	35.1	1137	6	ABL58400 Human lar
34	1063.4	32.9	1115	8	ACC49021 ABC1 gene
35	996.4	30.8	1033	8	ACC49024 ABC1 gene
36	899.2	27.8	900	12	ADJ77896 Phenotype
37	899.2	27.8	900	12	ADJ77895 Phenotype
38	377.6	11.7	156043	12	ADL08127 Human gen
39	350.4	10.8	79544	12	ADQ97764 Human can
40	336.4	10.4	151909	14	ABE96535 Human CAB
41	336	10.4	763	4	AAH04729 Human cDN
42	336	10.4	1750	4	AAH17451 Human cDN
43	333	10.3	80928	12	ADO25290 Human pro
44	330.8	10.2	20645	4	AAI05355 Human rep
45	330.8	10.2	20645	4	ABL98224 Human tes

#### ALIGNMENTS

RESULT 1

AAD37265

ID AAD37265 standard; DNA; 3231 BP.

XX AAD37265;

XX 21-AUG-2002 (first entry)

XX Human ABC1 transcription regulatory DNA #1.

XX Human; ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis; cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.

XX Homo sapiens.

XX WO200183746-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-EP005488.

XX 02-MAY-2000; 2000US-0201280P.

XX (AVET ) AVENTIS PHARMA SA.

XX Rosier-Montus M, Prades C, Lemoine C, Naudin L, Deneffe P;

XX Brewer B, Duverger N, Remaley A, Santamarina-Pojo S;

XX WPI; 2002-154404/20.

XX Isolated nucleic acid useful for modifying the ATP-binding cassette 1 (ABC1) and screening for candidate modulatory compounds or substances.

XX Claim 1; Page 130-131; 152pp; English.

XX The invention relates a nucleic acid which is capable of regulating the transcription of human ATP-binding cassette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholesterol metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABC1 gene. They are used in antisense therapy. Compositions comprising sequences of the

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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 22:47:42 ; Search time 858.843 Seconds  
(without alignments)  
3382.690 Million cell updates/sec

Title: US-09-846-456A-1

Perfect score: 3231

Sequence: 1 acaggcatgtgagcagtg.....gccccacatccccaccatt 3231

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/pubna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubna/PCT\_NEW\_PUB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubna/US09\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubna/US10\_NEW\_PUB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubna/US10\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubna/US11\_NEW\_PUB.seq.\*
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- 11: /cgn2\_6/ptodata/1/pubna/US11\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	3182	98.5	159138	7 US-10-995-561-13230	Sequence 13230, A
2	334.8	10.4	169725	11 US-11-121-086-63	Sequence 63, Appl
3	334.6	10.4	189539	11 US-11-121-086-16	Sequence 16, Appl
4	330.4	10.2	189539	11 US-11-121-086-16	Sequence 16, Appl
5	330	10.2	305312	7 US-10-995-561-13236	Sequence 13236, A
6	327.8	10.1	141121	7 US-10-995-561-13262	Sequence 13262, A
7	322.6	10.0	92600	7 US-10-857-780-1	Sequence 1, Appl
8	322.2	10.0	141121	7 US-10-995-561-13262	Sequence 13262, A
9	322	10.0	148935	7 US-10-995-561-13308	Sequence 13308, A
10	321.8	10.0	27509	7 US-10-995-561-13319	Sequence 13319, A
11	321.4	9.9	100001	7 US-10-944-272-1	Sequence 1, Appl
12	321.4	9.9	100001	11 US-11-096-191-718	Sequence 718, Appl
13	321	9.9	79528	7 US-10-276-233A-6	Sequence 6, Appl
14	318.8	9.9	51917	7 US-10-995-561-13338	Sequence 13338, A
15	317.2	9.8	161994	11 US-11-112-908-57	Sequence 57, Appl
16	314.2	9.7	159695	11 US-11-121-086-56	Sequence 56, Appl
17	314	9.7	135019	7 US-10-849-438-11	Sequence 11, Appl
18	307.2	9.5	79528	7 US-10-276-233A-6	Sequence 6, Appl
19	307.2	9.5	86081	7 US-10-995-561-13246	Sequence 13246, A
20	306.4	9.5	199321	11 US-11-121-086-10	Sequence 10, Appl
21	306	9.5	86950	7 US-10-857-780-5	Sequence 5, Appl

22	305.8	9.5	1080000	7 US-10-928-446A-1	Sequence 1, Appl
23	305.8	9.5	1080000	7 US-10-928-446A-181	Sequence 181, App
24	305.8	9.5	1080000	7 US-10-928-446A-183	Sequence 183, App
25	305.8	9.5	1080000	7 US-10-928-446A-185	Sequence 185, App
26	305.8	9.5	1080000	7 US-10-928-446A-187	Sequence 187, App
27	305.8	9.5	1080000	7 US-10-928-446A-189	Sequence 189, App
28	305.8	9.5	1080000	7 US-10-928-446A-191	Sequence 191, App
29	305.8	9.5	1080000	7 US-10-928-446A-193	Sequence 193, App
30	305.8	9.5	1080000	7 US-10-928-446A-195	Sequence 195, App
31	305.8	9.5	1080000	7 US-10-928-446A-197	Sequence 197, App
32	305.8	9.5	1080000	7 US-10-928-446A-199	Sequence 199, App
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34	303.8	9.4	161874	11 US-11-121-086-75	Sequence 75, Appl
35	303.2	9.4	149419	11 US-11-112-908-49	Sequence 49, Appl
36	303.2	9.4	161726	11 US-11-112-908-48	Sequence 48, Appl
37	303.2	9.4	161726	11 US-11-112-908-52	Sequence 52, Appl
38	303.2	9.4	166111	11 US-11-112-908-47	Sequence 47, Appl
39	303	9.4	175023	11 US-11-121-086-18	Sequence 18, Appl
40	302.6	9.4	135019	7 US-10-849-438-11	Sequence 11, Appl
41	302.4	9.4	175416	11 US-11-121-086-43	Sequence 43, Appl
42	302	9.3	67088	7 US-10-995-561-13365	Sequence 13365, A
43	302	9.3	160226	11 US-11-121-086-29	Sequence 29, Appl
44	301.4	9.3	165857	11 US-11-121-086-34	Sequence 34, Appl
45	300.6	9.3	215308	11 US-11-121-086-77	Sequence 77, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-995-561-13230  
; Sequence 13230, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13230  
; LENGTH: 159138  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(159138)  
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables  
US-10-995-561-13230

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Best Local Similarity	98.6%	Pred. No. 0;		
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QY	2	CAGGGCATGTGGCAGGTGCTGTAATCTCAAGTTACTCGGAGGTGGAGGTTCGAATCAG	61	
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DB	3156	CCAGATGCGACCAATTCACCTCCAGCTGGGCAACAAAGGTGAACCTCCATCTCAATTA	3215	
QY	122	AAAAAAAAGAAATGATTTGGTGGTGCATTCCTCAATAGGTAGGAGAGAGAGAGAGGA	181	
DB	3216	AAAAAAAAGAAATGATTTGGTGGTGCATTCCTCAATAGGTAGGAGAGAGAGAGAGGA	3275	
QY	182	GATGAGGTGAGGAGATCTTAATCTCTTAATCTAGGAGAGAGAGAGAGAGAGAGG	241	
DB	3276	GATGAGGTGAGGAGATCTTAATCTCTTAATCTAGGAGAGAGAGAGAGAGAGAGG	3335	

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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 19:02:01 ; Search time 1838.85 Seconds  
(without alignments)  
14529.947 Million cell updates/sec

Title: US-09-846-456A-1

Perfect score: 3231

Sequence: 1 acaggcatgtggcagggtg.....gccccacacccccaccactt 3231

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA Main:  
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2: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubna/US09\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubna/US09A\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubna/US10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	3231	100.0	3231	3	US-09-846-456-1		Sequence 1, Appli
2	3231	100.0	3231	3	US-09-846-456-1		Sequence 3, Appli
3	3179.6	98.4	159138	8	US-10-719-993-6777		Sequence 6777, Ap
4	3179.6	98.4	159138	8	US-10-741-600-17613		Sequence 17613, A
5	3127.8	96.8	183999	7	US-10-745-377-1		Sequence 1, Appli
6	3127.8	96.8	183999	7	US-10-872-113-1		Sequence 1, Appli
7	2893	89.5	2893	3	US-09-846-456-3		Sequence 3, Appli
8	2893	89.5	2893	3	US-09-846-456-3		Sequence 23, Appli
9	2891.4	89.5	2893	3	US-09-846-827-23		Sequence 137, App
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12	2891.4	89.5	2893	3	US-09-846-827-140		Sequence 141, App
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14	2891.4	89.5	2893	3	US-09-846-827-142		Sequence 143, App
15	2891.4	89.5	2893	3	US-09-846-827-143		Sequence 144, App
16	2891.4	89.5	2893	3	US-09-846-827-144		Sequence 145, App
17	2891.4	89.5	2893	3	US-09-846-827-145		Sequence 146, App
18	2891.4	89.5	2893	3	US-09-846-827-146		Sequence 147, App
19	2891.4	89.5	2893	3	US-09-846-827-148		Sequence 149, App
20	2891.4	89.5	2893	3	US-09-846-827-149		Sequence 150, App
21	2891.4	89.5	2893	3	US-09-846-827-150		Sequence 151, App
22	2891.4	89.5	2893	3	US-09-846-827-151		Sequence 152, App
23	2891.4	89.5	2893	3	US-09-846-827-154		Sequence 155, App

## ALIGNMENTS

## RESULT 1

US-09-846-456-1  
; Sequence 1, Application US/09846456

; Patent No. US20020146792A1

; GENERAL INFORMATION:

; APPLICANT: Rosier, Marie

; APPLICANT: Prades, Catherine

; APPLICANT: Lemoine, Cendrine

; APPLICANT: Naudin, Laurent

; APPLICANT: Deneffe, Patrice

; APPLICANT: Duverger, Nicolas

; APPLICANT: Brewer, Bryan

; APPLICANT: Remaley, Alan

; APPLICANT: Pojo, Silvia

; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying

; TITLE OF INVENTION: Activity and Therapeutic Uses

; FILE REFERENCE: 3806.0505

; CURRENT APPLICATION NUMBER: US/09/846.456

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/201,280

; PRIOR FILING DATE: 2000-05-02

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 1

; LENGTH: 3231

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-846-456-1

Query Match 100.0%; Score 3231; DB 3; Length 3231;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3231; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 ACAGGCATGTGGCAGGTGCTCTAATCTCAGTTACTTCGGGAGGTGGAGTTGCAATGA 60

Db 1 ACAGGCATGTGGCAGGTGCTCTAATCTCAGTTACTTCGGGAGGTGGAGTTGCAATGA 60

Qy 61 GCCCAGATCGCACCATTCGCTCCAGCTGGGCAACAAAGGTGAAATCCATCTCAATT 120

Db 61 GCCCAGATCGCACCATTCGCTCCAGCTGGGCAACAAAGGTGAAATCCATCTCAATT 120

Qy 121 AAAAAAAGAAATGATTTTGGTGGTCCACTTCGCTGGGCAACAAAGGTGAAATCCATCTCAATT 180

Db 121 AAAAAAAGAAATGATTTTGGTGGTCCACTTCGCTGGGCAACAAAGGTGAAATCCATCTCAATT 180

Qy 181 AGATGGAGGGTCAGGAGATCTAATTAATCTCTTAAATATCATGCTAGGAAAGATAACACCT 240

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Qy 181 AGATGGAGGGTCAGGAGATCTAATTAATCTCTTAAATATCATGCTAGGAAAGATAACACCT 240

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Db 181 AGATGGAGGGTCAGGAGATCTAATTAATCTCTTAAATATCATGCTAGGAAAGATAACACCT 240

Qy 181 AGATGGAGGGTCAGGAGATCTAATTAATCTCTTAAATATCATGCTAGGAAAGATAACACCT 240

Db 181 AGATGGAGGGTCAGGAGATCTAATTAATCTCTTAAATATCATGCTAGGAAAGATAACACCT 240

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 06:52:37 ; Search time 20.1384 Seconds  
(without alignments)  
14034.494 Million cell updates/sec

Title: US-09-846-456A-5

Perfect score: 159

Sequence: 1 ttaatgaccgacccagggcg.....ctttcagaagaagacaaca 159

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*  
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7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155.8	98.0	10442	3	US-09-596-141C-1
2	155.8	98.0	10442	3	US-09-595-526C-1
3	155.8	98.0	10474	3	US-09-596-141C-7
4	155.8	98.0	10474	3	US-09-596-141C-9
5	155.8	98.0	10474	3	US-09-595-526C-7
6	155.8	98.0	10474	3	US-09-595-526C-9
7	142.2	89.4	447	3	US-09-621-976-13889
8	142.2	89.4	1062	3	US-10-000-489-101
9	142.2	89.4	10545	3	US-09-526-193A-14
10	135.2	85.0	7860	3	US-09-526-193A-2
11	35.8	22.5	234884	3	US-09-949-016-16420
12	35	22.0	298	3	US-09-513-999C-10257
13	34.6	21.8	8920	3	US-09-949-016-15145
14	34.6	21.8	30678	3	US-09-949-016-15145
15	33.2	20.9	6588	3	US-09-949-016-1076
16	32.8	20.6	137753	3	US-09-949-016-17404
17	32.6	20.5	601	3	US-09-949-016-112405
18	32.6	20.5	601	3	US-09-949-016-112406
19	32.6	20.5	86380	3	US-09-949-016-14837
20	30.6	19.2	2935	3	US-09-976-594-365
21	30.6	19.2	8961	3	US-09-949-016-15910
22	30.4	19.1	390	3	US-09-489-039A-7103
23	30.4	19.1	485	3	US-09-513-999C-1002
24	30.4	19.1	532	3	US-09-513-999C-1003

25 30.4 19.1 2028 3 US-09-949-016-2675  
26 30.4 19.1 36223 3 US-09-949-016-14417  
27 30.2 19.0 1727 3 US-09-327-983-3  
28 30.2 19.0 1727 3 US-09-549-827A-7  
29 30.2 19.0 118999 3 US-09-791-1058-32  
30 30.2 19.0 118999 3 US-09-735-271-884  
31 30 18.9 4771 2 US-08-866-650-2  
32 30 18.9 4771 2 US-09-021-287-2  
33 30 18.9 4771 2 US-09-240-473-2  
34 30 18.9 33529 3 US-09-144-085-3  
35 29.8 18.7 11359 3 US-09-949-016-17575  
36 29.8 18.7 118999 3 US-09-791-1058-32  
37 29.6 18.6 425 3 US-09-621-976-1009  
38 29.6 18.6 22761 3 US-09-902-540-1219  
39 29.4 18.5 364 3 US-09-621-976-17202  
40 29.4 18.5 373 3 US-09-513-999C-12849  
41 29.4 18.5 3147 2 US-08-781-802-7  
42 29.4 18.5 3147 3 US-08-694-078-7  
43 29.4 18.5 3147 3 US-09-058-260-7  
44 29.4 18.5 26640 3 US-09-949-016-17431  
45 29.2 18.4 14967 3 US-09-949-016-15448

ALIGNMENTS

RESULT 1

US-09-596-141C-1  
; Sequence 1, Application US/09596141C  
; Patent No. 6821774  
; GENERAL INFORMATION:  
; APPLICANT: Lawn, Richard M.  
; APPLICANT: Wade, David  
; APPLICANT: Oram, John F.  
; APPLICANT: Garvin, Michael  
; TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol Efflux and Raising HDL using APP Binding Cassette  
; TITLE OF INVENTION: Transporter Protein ABC1  
; FILE REFERENCE: 99,395-B  
; CURRENT APPLICATION NUMBER: US/09/596,141C  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/140,264  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: US 60/153,872  
; PRIOR FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: US 60/166,573  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO 1  
; LENGTH: 10442  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(10442)  
; OTHER INFORMATION: All n's are unknown.  
US-09-596-141C-1

Query Match 98.0%; Score 155.8; DB 3; Length 10442;  
Best Local Similarity 98.7%; Pred. No. 8.6e-36;  
Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DB 198 TTAATGACCAAGCAGCGCGCTCCCTGTCAGCTCTGGCGCGCTTCCTTCAGGGCTCCC 257  
QY 61 GAGCCACACGCTGGCGCTGCTGGCTAGGGAACATGGCATGTTGGCTCAGCTAGGTTG 120  
DB 258 GAGCCACACGCTGGCGCTGCTGGCTAGGGAACATGGCTTGTGGCTCAGCTAGGTTG 317  
QY 121 CTGCTGGAGAGACCTTTCACATTTTCAGAGAGACAAACA 159  
DB 318 CTGCTGGAGAGACCTTTCACATTTTCAGAGAGACAAACA 356

Result No.	Score	Match	Query	ID	Description
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2	203.8	57.1	1062	3	US-10-000-489-101
3	203.4	57.0	447	3	US-09-621-976-13889
4	159.4	44.6	10442	3	US-09-596-141C-1
5	159.4	44.6	10442	3	US-09-595-526C-1
6	159.4	44.6	10474	3	US-09-596-141C-7
7	159.4	44.6	10474	3	US-09-596-141C-9
8	159.4	44.6	10474	3	US-09-595-526C-7
9	159.4	44.6	10474	3	US-09-595-526C-9
10	135.8	38.0	7860	3	US-09-526-193A-2
11	37.8	10.6	8920	3	US-09-949-016-15145
12	37.8	10.6	30678	3	US-09-949-016-12818
C 13	36.4	10.2	154600	3	US-09-949-016-14757
C 14	35.8	10.0	858	3	US-09-540-236-1287
C 15	35.8	10.0	92407	3	US-09-596-002-36
C 16	35.8	10.0	234884	3	US-09-949-016-15420
C 17	35.2	9.9	601	3	US-09-949-016-21645
C 18	35.2	9.9	601	3	US-09-949-016-156690
C 19	35.2	9.9	231129	3	US-09-949-016-16110
C 20	35.2	9.9	266293	3	US-09-949-016-11934
21	35	9.8	298	3	US-09-513-999C-10257
22	34.4	9.6	6588	3	US-09-949-016-1076
23	33.4	9.4	4438	3	US-09-949-016-13578
24	32.8	9.2	137753	3	US-09-949-016-17404

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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 06:52:37 ; Search time 366,418 Seconds  
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14034.494 Million cell updates/sec

Title: US-09-846-456A-3

Perfect score: 2893

Sequence: 1 acagggcatggtggcagggtg.....ctagtcggcgcaaaaacccc 2893

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/PCUS COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/ina/backfilesi.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1394.4	48.2	1643	US-09-596-141C-3	Sequence 3, Appli
2	1394.4	48.2	1643	US-09-595-526C-3	Sequence 3, Appli
3	1027.8	35.5	1197	US-09-560-372-1	Sequence 1, Appli
4	347.4	12.0	118143	US-09-949-016-17196	Sequence 17196, A
5	335.6	11.6	13821	US-09-949-016-13690	Sequence 13690, A
6	333	11.5	84870	US-09-949-016-17547	Sequence 17547, A
7	330.4	11.4	36148	US-09-949-016-12969	Sequence 12969, A
8	330	11.4	14519	US-09-949-016-15611	Sequence 15611, A
9	330	11.4	14519	US-09-949-016-15612	Sequence 15612, A
10	325.2	11.2	31318	US-09-949-016-12495	Sequence 12495, A
11	325.2	11.2	31319	US-09-949-016-15963	Sequence 15963, A
12	324.8	11.2	87734	US-09-949-016-17521	Sequence 17521, A
13	324.4	11.2	78630	US-09-949-016-16790	Sequence 16790, A
14	323.4	11.2	44019	US-09-949-016-14902	Sequence 14902, A
15	321.6	11.1	9208	US-09-949-016-15567	Sequence 15567, A
16	321.2	11.1	786431	US-09-751-389-3	Sequence 3, Appli
17	319.2	11.0	4441	US-09-949-016-15325	Sequence 15325, A
18	319	11.0	11543	US-09-949-016-12071	Sequence 12071, A
19	319	11.0	11543	US-09-949-016-12673	Sequence 12673, A
20	319	11.0	11544	US-09-949-016-16172	Sequence 16172, A
21	319	11.0	11544	US-09-949-016-16173	Sequence 16173, A
22	319	11.0	11544	US-09-949-016-16174	Sequence 16174, A
23	319	11.0	11544	US-09-949-016-16175	Sequence 16175, A
24	318.2	11.0	37292	US-09-949-016-15382	Sequence 15382, A

25	318	11.0	40091	3	US-09-949-016-16011	Sequence 16011, A
26	317.2	11.0	26314	3	US-09-949-016-16389	Sequence 16389, A
27	317	11.0	124264	3	US-09-949-016-16396	Sequence 16396, A
28	316.8	11.0	53442	3	US-09-949-016-11921	Sequence 11921, A
29	316.8	11.0	53453	3	US-09-949-016-13370	Sequence 13370, A
30	316.6	10.9	47347	3	US-09-949-016-14130	Sequence 14130, A
31	316.6	10.9	49721	3	US-09-949-016-17538	Sequence 17538, A
32	316.6	10.9	100463	3	US-09-949-016-12511	Sequence 12511, A
33	316.6	10.9	100468	3	US-09-949-016-13725	Sequence 13725, A
34	315.6	10.9	84252	3	US-09-949-016-17315	Sequence 17315, A
35	315.4	10.9	55114	3	US-09-949-016-16792	Sequence 16792, A
36	315.4	10.9	116592	3	US-09-818-512-3	Sequence 3, Appli
37	315.4	10.9	116592	3	US-10-354-065-3	Sequence 3, Appli
38	315.2	10.9	75929	3	US-09-949-016-15543	Sequence 15543, A
39	315.2	10.9	75929	3	US-09-949-016-15544	Sequence 15544, A
40	314.6	10.9	91831	3	US-09-949-016-13694	Sequence 13694, A
41	314.4	10.9	23932	3	US-09-949-016-16099	Sequence 16099, A
42	313.8	10.8	25401	3	US-09-949-016-13345	Sequence 13345, A
43	313.6	10.8	118143	3	US-09-949-016-17196	Sequence 17196, A
44	312.8	10.8	55114	3	US-09-949-016-16792	Sequence 16792, A
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## ALIGNMENTS

## RESULT 1

US-09-596-141C-3  
; Sequence 3, Application US/09596141C  
; Patent No. 6821774  
; GENERAL INFORMATION:  
; APPLICANT: Lawn, Richard M.  
; APPLICANT: Wade, David  
; APPLICANT: Oram, John F.  
; APPLICANT: Garvin, Michael  
; TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol Efflux and Raising HDL using ATP Binding Cassette  
; TITLE OF INVENTION: Transporter Protein ABC1  
; FILE REFERENCE: 99,395-B  
; CURRENT APPLICATION NUMBER: US/09/596,141C  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/140,264  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: US 60/153,872  
; PRIOR FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: US 60/166,573  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO 3  
; LENGTH: 1643  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-596-141C-3

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Best Local Similarity 97.9%; Pred. No. 0;  
Matches 1524; Conservative 0; Mismatches 6; Indels 26; Gaps 10;  
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Db 16 GGTCCACATGCACTTCCAGGGCTGCTTTGG--CTCTTCTATGCGTCTGTCTGAGTGT 73  
QY 1405 GATAGAACCACTGATGTGAGTACCTGGCTTGAGCGCTGGCTGGAGATCCTGTTGACTG 1464  
Db 74 GATAGAACCACTGATGTGAGTACCTGGCTTGAG--CTGCGCTGGAGATCCTGTTGACTG 132  
QY 1465 TAGCATGGAGGGGGCTTGTGACGTCAATGTCTGATGACAGGTGGTGGAGTCTTGAAT 1524  
Db 133 TAGCATGGAGGGGGCTTGT--CAGCTGAATGTCTGATGACAGGTGGTGGAGTCTTGAAT 191  
QY 1525 ATGATGAGCTGAGGTGGGAAGAGAGTAGGCTTGGGGCAGCTCTCTCATGCCACTCA 1584  
Db 192 ATGATGAGCTGAGGTGGGAAGAGAGTAGGCTTGGGGCAGCTCTCTCATGCCACTCA 251



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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 06:52:37 ; Search time 409.228 Seconds  
(without alignments)  
14034.494 Million cell updates/sec

Title: US-09-846-456A-1

Perfect score: 3231

Sequence: 1 acagggcatgtggcagggtg.....gccccacatccccaccactt 3231

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*  
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2: /cgm2\_6/ptodata/1/ina/5 COMB.seq.\*  
3: /cgm2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgm2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgm2\_6/ptodata/1/ina/H COMB.seq.\*  
6: /cgm2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
7: /cgm2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgm2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgm2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1485.4	46.0	1643	US-09-596-141C-3	Sequence 3, Appli
2	1485.4	46.0	1643	US-09-595-526C-3	Sequence 3, Appli
3	1134.8	35.1	1197	US-09-560-372-1	Sequence 1, Appli
4	347.4	10.8	118143	US-09-949-016-17196	Sequence 17196, A
5	335.6	10.4	13821	US-09-949-016-13690	Sequence 13690, A
6	333	10.3	84870	US-09-949-016-17547	Sequence 17547, A
7	330.4	10.2	36148	US-09-949-016-12969	Sequence 12969, A
8	330	10.2	14519	US-09-949-016-15611	Sequence 15611, A
9	330	10.2	14519	US-09-949-016-15612	Sequence 15612, A
10	325.2	10.1	31318	US-09-949-016-12495	Sequence 12495, A
11	325.2	10.1	31319	US-09-949-016-15963	Sequence 15963, A
12	324.8	10.1	87734	US-09-949-016-17521	Sequence 17521, A
13	324.8	10.0	78630	US-09-949-016-16790	Sequence 16790, A
14	323.4	10.0	44019	US-09-949-016-14902	Sequence 14902, A
15	321.6	10.0	9208	US-09-949-016-15567	Sequence 15567, A
16	321.2	9.9	786431	US-09-751-389-3	Sequence 3, Appli
17	319.2	9.9	4441	US-09-949-016-15325	Sequence 15325, A
18	319	9.9	11543	US-09-949-016-12071	Sequence 12071, A
19	319	9.9	11543	US-09-949-016-12673	Sequence 12673, A
20	319	9.9	11544	US-09-949-016-16172	Sequence 16172, A
21	319	9.9	11544	US-09-949-016-16173	Sequence 16173, A
22	319	9.9	11544	US-09-949-016-16174	Sequence 16174, A
23	319	9.9	11544	US-09-949-016-16175	Sequence 16175, A
24	318.2	9.8	37292	US-09-949-016-15382	Sequence 15382, A

## ALIGNMENTS

## RESULT 1

US-09-596-141C-3  
; Sequence 3, Application US/09596141C  
; Patent No. 6821774  
; GENERAL INFORMATION:  
; APPLICANT: Lawn, Richard M.  
; APPLICANT: Wade, David  
; APPLICANT: Oram, John P.  
; APPLICANT: Garvin, Michael  
; TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol Efflux and Raising HDL using ATP Binding Cassette Transporter Protein ABC1  
; TITLE OF INVENTION: Efflux and Raising HDL using ATP Binding Cassette Transporter Protein ABC1  
; FILE REFERENCE: 99,395-B  
; CURRENT APPLICATION NUMBER: US/09/596,141C  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/140,264  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: US 60/153,872  
; PRIOR FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: US 60/166,573  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO 3  
; LENGTH: 1643  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-596-141C-3

Query Match 46.0%; Score 1485.4; DB 3; Length 1643;  
Best Local Similarity 98.1%; Pred. No. 0;  
Matches 1615; Conservative 0; Mismatches 6; Indels 26; Gaps 10;  
Qy 1345 GCCTCCACATGCACTTCCAGGGCTGCTGGGCTCTTCTATGCGTCTGCTGAGTGT 1404  
Db 16 GGCTCCACATGCACTTCCAGGGCTGCTGGGCTCTTCTATGCGTCTGCTGAGTGT 73  
Qy 1405 GATAGACCACTGATGTGAGTACTGGCTTGGCTGAGCTGCTGAGCTGCTGAGTGT 1464  
Db 74 GATAGACCACTGATGTGAGTACTGGCTTGGCTGAGCTGCTGAGTGT 132  
Qy 1465 TAGCATGGAGGGCTTGTGCGTGAATGTGCTGAGCTGCTGAGTGTGCTGAGTGT 1524  
Db 133 TAGCATGGAGGGCTTGT-CAGCTGAATGTGCTGAGTGTGCTGAGTGTGCTGAGTGT 191  
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